<u>In the Specification:</u>

<u>On page 1, please amend the "Related Applications" paragraph (lines 5-8) as follows:</u>

<u>This application is a divisional application of U.S. Application Serial No. 10/023,515, filed on December 18, 2001, which</u> ~~This application~~ claims priority to U.S. [[p]]<u>P</u>rovisional [[a]]<u>A</u>pplication Serial ~~number~~ <u>No.</u> 60/256,369, filed on December 18, 2000, and U.S. [[p]]<u>P</u>rovisional [[a]]<u>A</u>pplication Serial ~~number~~ <u>No.</u> 60/279,508, filed on March 28, 2001, the contents of which are ~~incorporated herein by reference~~ <u>hereby incorporated herein by reference in their entirety</u>.

<u>Please amend the paragraph on page 2 lines 13-28 to read as follows:</u>

Accordingly, in one aspect, the invention features a nucleic acid molecule that encodes a 53010 protein or polypeptide, e.g., a biologically active portion of the 53010 protein. In a preferred embodiment the isolated nucleic acid molecule encodes a polypeptide having the amino acid sequence of SEQ ID NO:2. In other embodiments, the invention provides isolated 53010 nucleic acid molecules having the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, a full complement of SEQ ID NO:1 or SEQ ID NO:3~~, or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number____~~. In still other embodiments, the invention provides nucleic acid molecules that are substantially identical (e.g., naturally occurring allelic variants) to the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3~~, or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number____~~. In other embodiments, the invention provides a nucleic acid molecule which hybridizes under a stringency condition described herein to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, ~~or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number____~~, wherein the nucleic acid encodes a full length 53010 protein or an active fragment thereof.

<u>Please amend the paragraph on page 3, lines 15-25 to read as follows:</u>

In other embodiments, the invention provides 53010 polypeptides, e.g., a 53010 polypeptide having the amino acid sequence shown in SEQ ID NO:2 or ~~the amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC Accession Number____~~; an amino acid sequence that is substantially identical to the amino acid sequence shown in SEQ ID NO:2 ~~or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC Accession Number____~~; or an amino acid sequence encoded by a nucleic acid molecule having a nucleotide sequence which hybridizes under a stringency condition described

herein to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, ~~or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number~~____, wherein the nucleic acid encodes a full length 53010 protein or an active fragment thereof.

Please amend the paragraph on page 9, lines 22-24 to read as follows:

For general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer *et al.* (1997) *Protein* 28:405-420 and [[http://]]www.psc.edu/general/ software/packages/pfam/pfam.html.

Please delete the paragraph on page 9, lines 25-31

~~A plasmid containing the nucleotide sequence encoding human 53010 (clone "Fbh53010FL") was deposited with American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA 20110-2209, on ____ and assigned Accession Number _____. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. This deposit was made merely as a convenience for those of skill in the art and is not an admission that a deposit is required under 35 U.S.C. §112.~~

Please amend the paragraph on page 11, lines 10-25 to read as follows:

To identify the presence of a "carboxylesterase" domain in a 53010 protein sequence, and make the determination that a polypeptide or protein of interest has a particular profile, the amino acid sequence of the protein can be searched against the Pfam database of HMMs (e.g., the Pfam database, release 2.1) using the default parameters ([[http://]]www.sanger.ac.uk/Software/Pfam/HMM_search). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for MILPAT0063 and a score of 15 is the default threshold score for determining a hit. Alternatively, the threshold score for determining a hit can be lowered (e.g., to 8 bits). A description of the Pfam database can be found in Sonhammer *et al.* (1997) *Proteins* 28(3):405-420 and a detailed description of HMMs can be found, for example, in Gribskov *et al.*(1990) *Meth. Enzymol.* 183:146-159; Gribskov *et al.*(1987) *Proc. Natl. Acad. Sci. USA* 84:4355-4358; Krogh *et al.*(1994) *J. Mol. Biol.* 235:1501-1531; and Stultz *et al.*(1993) *Protein Sci.* 2:305-314, the contents of which are incorporated herein by reference. A search was

performed against the HMM database resulting in the identification of a "carboxylesterase" domain in the amino acid sequence of human 53010 at about residues 44 to 545 of SEQ ID NO:2 (see Figure 2).

Please amend the paragraph on page 21, lines 10-23 to read as follows:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch ((1970) *J. Mol. Biol.* 48:444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at [[http://]]www.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at [[http://]]www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used unless otherwise specified) are a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

Please amend the paragraph beginning on page 21, line 28 to read as follows:

The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 53010 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to 53010 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25:3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See [[http://]]www.ncbi.nlm.nih.gov.